

AMENDMENTS TO THE CLAIMS

This listing replaces all prior versions and listings of claims in the application.

Listing of Claims

1 – 24 (Previously Cancelled)

25. (Currently Amended) [A novel] An amylase [which] that comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 6, SEQ ID NO: 8, and an equivalent thereof, wherein said amylase acts on a substrate saccharide, the substrate saccharide being composed of at least three sugar units wherein at least three sugar units from the reducing end are glucose residues, so as to liberate principally monosaccharides and/or disaccharides by hydrolyzing the substrate saccharide from the reducing end side.

26. (Currently Amended) The [novel] amylase claimed in Claim 25[which has a principal activity of acting on a substrate saccharide], wherein the substrate saccharide [being] is composed of at least three sugar units, wherein at least three sugar units from the reducing end side are glucose residues, and wherein the linkage between the first and the second glucose residues from the reducing end side is α -1, α -1 while the linkage between the second and the third glucose residues from the reducing end side is α -1,4, [so as to liberate] such that said amylase liberates α , α -trehalose by hydrolyzing the α -1,4 linkage between the second and the third glucose residues.

27. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein said amylase also has an activity of endotype-hydrolyzing one or more α -1,4 linkages within the molecular chain of a substrate.

28. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein said amylase has an activity of hydrolyzing a substrate trehaloseoligosaccharide [such as glucosyltrehalose and maltooligosyltrehalose] at the α -1,4 linkage between the second and the third glucose residues from the reducing end side to liberate α , α -trehalose.

29. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein its molecular weight measured by SDS-polyacrylamide gel electrophoresis is 61,000 to 64,000, [approximately].

30. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein the amylase has the following physical and chemical properties:

- (1) Optimum pH with in the range from 4.5 to 5.5;
- (2) Optimum temperature within the range from 60 to 85°C;
- (3) pH stability within the range from 4.0 to 10.0; and
- (4) Thermostability which allow 100% enzymatic activity to remain even after exposure at 80°C for 6 hours.

31. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein the isoelectric point measured by isoelectric focusing is pH 4.3 to pH 5.4.

32. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein its activity can be fully inhibited with 5 mM CuSO₄.

33. (Currently Amended) The [novel] amylase claimed in Claim 25, wherein the amylase is derived from an archaebacterium belonging to the order *Sulfolobales*.

34. (Currently Amended) The [novel] amylase claimed in Claim 33, wherein the amylase is derived from an archaebacterium belonging to the genus *Sulfolobus*.

35. (Currently Amended) The [novel] amylase claimed in Claim 34, wherein the archaebacterium belonging to the genus *Sulfolobus* is the *Sulfolobus solfataricus* strain KM1 (FERM BP-4626) [or a variant thereof].

36. (Currently Amended) The [novel] amylase claimed in Claim 34, wherein the archaebacterium belonging to the genus *Sulfolobus* is the *Sulfolobus solfataricus* strain DSt4 5833 [or a variant thereof].

37. (Currently Amended) The [novel] amylase claimed in Claim 34, wherein the archaeobacterium belonging to the genus *Sulfolobus* is the *Sulfolobus acidocaldarius* strain ATCC 33909 [or a variant thereof].

38 – 122 (Previously Cancelled)

123. (Cancelled)

124. (Cancelled)

125. (Currently Amended) The [polypeptide] amylase claimed in Claim [123] 25, wherein said amino acid sequence further [comprising] comprises Met at the N terminus.

126. (Cancelled)

127. (Cancelled)

128. (Cancelled)

129. (New) The amylase claimed in Claim 28, wherein the substrate is at least one of glucosyltrehalose and maltooligosyltrehalose